

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 08:38:11 ; Search time 195 Seconds
(without alignments)

436.695 Million cell updates/sec

Title: US-10-723-368-2

Perfect score: 794

Sequence: 1 MARIPYALGICSLICLQLP.....GPAGRQDSAPVDPSPSHYS 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	794	100.0	148	1	ADM2_HUMAN	Q7z4h4 homo sapien
2	455	57.3	150	1	ADM2_MOUSE	Q7tnk8 mus musculu
3	451	56.8	146	1	ADM2_RAT	P61312 rattus norv
4	451	56.8	146	2	AA01302	Aa01302 rattus no
5	219.5	27.6	168	2	Q75XW7	Q75xw7 fugu rubrip
6	219.5	27.6	168	2	BAD02342	Ba02342 fugu rubr
7	204	25.7	159	2	Q75XW6	Q75xw6 fugu rubrip
8	204	25.7	159	2	BAD02343	Ba02343 fugu rubr
9	201	25.3	140	2	Q61FS9	Q61fs9 brachydanio
10	99	12.5	186	2	Q8NF75	Q8nf75 homo sapien
11	98.5	12.4	953	2	Q6K769	Q6k769 oryza sativ
12	98.5	12.4	953	2	BAD21873	Ba21873 oryza sat
13	98.5	12.4	953	2	BAD21878	Ba21878 oryza sat
14	98	12.3	123	2	Q75XW4	Q75xw4 fugu rubrip
15	98	12.3	123	2	BAD02345	Ba02345 fugu rubr
16	98	12.3	1458	2	Q6BJT8	Q6bjt8 debarvomyce
17	98	12.3	2715	1	MLL4_HUMAN	Q9umh6 homo sapien
18	97.5	12.3	292	2	Q96RY6	Q96ry6 homo sapien
19	97.5	12.3	1003	1	MBD6_HUMAN	Q96dn6 homo sapien
20	97.5	12.3	1003	2	Q6P0P0	Q6p0p0 homo sapien
21	97.5	12.3	1003	2	AAH65530	AaH65530 homo sapi
22	97	12.2	174	2	Q75XW8	Q75xw8 fugu rubrip
23	97	12.2	174	2	BAD02341	Ba02341 fugu rubr
24	96.5	12.2	571	2	Q8NBL0	Q8nb10 homo sapien
25	96.5	12.2	1186	2	Q7T401	Q7t401 cercopithec
26	96	12.1	406	1	PYG2_HUMAN	Q9brq0 homo sapien
27	96	12.1	406	2	BAC03877	BaC03877 homo sapi
28	96	12.1	437	2	Q6Z8R8	Q6z8r8 oryza sativ
29	96	12.1	437	2	BAD10031	BaD10031 oryza sat
30	95.5	12.0	294	2	Q86TW3	Q86tw3 homo sapien
31	95.5	12.0	328	2	Q86TQ7	Q86tq7 homo sapien

32	95.5	12.0	414	2	Q6M1W2	Q6mlw2 corynebacte
33	95.5	12.0	414	2	CAF20925	CaF20925 corynebac
34	95.5	12.0	571	2	Q6H9L7	Q6h9l7 homo sapien
35	95	12.0	1829	1	X296_HUMAN	O15015 homo sapien
36	95	12.0	1832	2	Q8IVD8	Q8ivd8 homo sapien
37	94.5	11.9	201	2	Q9HAA0	Q9haa0 homo sapien
38	94	11.8	155	2	Q8PFC1	Q8pfc1 xanthomonas
39	94	11.8	171	2	Q6L8K5	Q6l8k5 cyprinus ca
40	94	11.8	171	2	BAD19046	BaD19046 cyprinus
41	94	11.8	756	2	Q6C2Z4	Q6c2z4 varrowia li
42	93.5	11.8	414	2	Q9SE59	Q9see9 arabidopsis
43	93.5	11.8	619	2	Q82IIL8	Q82il8 streptomyce
44	93	11.7	216	2	Q80VA6	Q80va6 mus musculu
45	93	11.7	500	1	FXE2_HUMAN	Q99526 homo sapien

ALIGNMENTS

RESULT 1	ADM2_HUMAN	STANDARD;	PRT;	148 AA.
ID	ADM2_HUMAN	STANDARD;	PRT;	148 AA.
AC	Q7Z4H4;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2 (Intermedin-long) (IMDL); Intermedin-short (IMDS)].			
GN	Name=ADM2; Synonyms=IM2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.			
RX	PubMed=14515490; DOI=10.1074/jbc.M30532200;			
RA	Roh J., Chang C.D., Bhalla A., Klein C., Hsu S.Y.T.;			
RT	"Intermedin is a calcitonin/calcitonin gene-related peptide family			
RT	peptide acting through the calcitonin receptor-like receptor/receptor			
RT	activity-modifying protein receptor complexes.";			
RL	J. Biol. Chem. 279:7264-7274(2004).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;			
RA	Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;			
RT	"Identification of novel adrenomedullin in mammals: a potent			
RT	cardiovascular and renal regulator.";			
RL	FEBS Lett. 556:53-58(2004).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;			
RA	Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,			
RA	Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,			
RA	Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,			
RA	Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Grafton D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Famlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.P., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.F.,			
RA	Mcclay J.C., McMurray A.A., Milne S.A., Mortimore B.J.,			
RA	Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,			
RA	Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,			
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,			
RA	Soderlund C., Spragon L., Steward C.A., Suleston J.E., Swann R.M.,			
RA	Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilning L.,			

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudo J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Rober A.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Phan Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chiesse S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Benis G., Bentley J., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
RA Sroussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -i- FUNCTION: IMDL and IMDS may play a role as physiological
CC regulators of gastrointestinal, cardiovascular bioactivities
CC mediated by the CALCR1/RAMPs receptor complexes. Activates the
CC CAMP-dependent pathway.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: Expressed in the esophagus, stomach, jejunum,
CC ileum, ileocecum, ascending colon, transverse colon, descending
CC colon and rectum.
CC -i- SIMILARITY: Belongs to the adrenomedullin family.
CC -----
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CC -----
CC EMBL; AF529213; AAC09100.1; -;
CC EMBL; AB121034; BAD07411.1; -;
CC EMBL; AL096767; -; NOT_ANNOTATED_CDS.
CC Genew; HGNC:28898; ADM2.
CC MIM; 608682; -;
CC AMidation; Cleavage on pair of basic residues; Hormone; Signal.
CC KW SIGNAL 1 24 Potential.
CC FT PROPEP 25 98 By similarity.
CC FT PEPTIDE 101 147 Adrenomedullin 2 (By similarity).
CC FT PEPTIDE 108 147 Intermedin-short (Potential).
CC FT DISULFID 110 115 By similarity.
CC FT MOD_RES 147 147 Tyrosine amide (G-148 provides amide
CC group) (Probable).
CC SQ SEQUENCE 148 AA; 15865 MW; 5E0E3098CFCE5BF2 CRC64;
CC -----
CC Query Match 100.0%; Score 794; DB 1; Length 148;
CC Best Local Similarity 100.0%; Pred. No. 2.2e-52;
CC Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC 1 MARIPAAAGCISLLCLQLPGSLGSRSGDPRPVKPREPPARSPSSSLQPRHPAPRVVW 60
CC |||||
CC 1 MARIPAAAGCISLLCLQLPGSLGSRSGDPRPVKPREPPARSPSSSLQPRHPAPRVVW 60
CC |||||
CC 61 KLHRAALQAGAGLAPVWGQPLRDGGHSGPRRHSGPRRTQALLRVGCVLTGCQVNL 120
CC |||||
CC 61 KLHRAALQAGAGLAPVWGQPLRDGGHSGPRRHSGPRRTQALLRVGCVLTGCQVNL 120
CC |||||
CC 121 SHRLWQLMGAGRQDSAPVDPSPHSYG 148
CC |||||
CC 121 SHRLWQLMGAGRQDSAPVDPSPHSYG 148
CC |||||

RESULT 2

ADM2 MOUSE
ID ADM2_MOUSE STANDARD; PRT; 150 AA.
AC Q7TNK9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
OS Name:ADM2; Synonyms:Am2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6;
RX PubMed=14615490; DOI=10.1074/jbc.M305332200;
RA Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;
RT "Intermedin is a calcitonin/calcitonin gene-related peptide family
RT peptide acting through the calcitonin receptor-like receptor/receptor
RT activity-modifying protein receptor complexes.";
RL J. Biol. Chem. 279:7264-7274(2004).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Kidney;
RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;
RA Takei Y., Inoue K., Ogoshi M., Kawahara T., Hannai H., Miyano S.;
RT "Identification of novel adrenomedullin in mammals: a potent
RT cardiovascular and renal regulator.";
RL FEBS Lett. 556:53-58(2004).
CC -i- FUNCTION: IMDL and IMDS may play a role as physiological
CC regulators of gastrointestinal, cardiovascular bioactivities
CC mediated by the CALCR1/RAMPs receptor complexes. Activates the
CC CAMP-dependent pathway.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: High expression detected in the submaxillary
CC gland, kidney, stomach, and mesentery, followed by the pituitary,
CC lung, pancreas, intestines, spleen, thymus and ovary. Expressed
CC mainly in the intermediate lobe of the pituitary, with sporadic in
CC the anterior lobe.
CC -i- SIMILARITY: Belongs to the adrenomedullin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF529212; AAC09099.1; -;
CC EMBL; AB121035; BAD07412.1; -;
CC MGD; MGI:2675256; Adm2.
CC AMidation; Cleavage on pair of basic residues; Hormone; Signal.
CC KW SIGNAL 1 25 Potential.
CC FT PROPEP 26 100 By similarity.
CC FT PEPTIDE 103 149 Adrenomedullin 2 (By similarity).
CC FT PEPTIDE 110 149 Intermedin-short (Potential).
CC FT DISULFID 112 117 By similarity.
CC FT MOD_RES 149 149 Tyrosine amide (G-150 provides amide
CC group) (Probable).
CC SQ SEQUENCE 150 AA; 16188 MW; 2BF392BFBFBDEBBA CRC64;
CC -----
CC Query Match 57.3%; Score 455; DB 1; Length 150;
CC Best Local Similarity 66.0%; Pred. No. 7.2e-27;
CC Matches 95; Conservative 12; Mismatches 35; Indels 2; Gaps 2;
CC -----
CC 6 TAAAGCISLLCLQLPGSLGSRSGDPRPVKPREPPARSPSSSLQPRHPAPRVVWKLHR- 64
CC |||||
CC 8 TATLGCISLLYL-LPGTISGLSGKGLRHRSRPPAPKIPSSNLQPGHPSLQPVVWKKRRH 66
CC |||||
CC 65 ALQAQRGAGLAPVWGQPLRDGGHSGPRRHSGPRRTQALLRVGCVLTGCQVNLSHRL 124
CC |||||

```
Db 67 APQPQGRGNALAMVHLHFGGSGSRHPGQRTGTSRRPAPHAQLLRVGCVLGTCCVQNLSHRL 126
QY 125 WOLMGPAQRDSAPVDPSPSPHSYG 148
Db 127 WOLVPSGRDSDAPVDPSPSPHSYG 150

RESULT 3
ADM2_RAT STANDARD; PRT; 146 AA.
AC F61312;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
GN Name=Adm2; Synonyms=Am2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;
RA Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.;
RT "Identification of novel adrenomedullin in mammals: a potent
RT cardiovascular and renal regulator.";
RL FEBS Lett. 556:53-58(2004).
RN [2]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=14615490; DOI=10.1074/jbc.M305332200;
RA Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;
RT "Intermedin is a calcitonin/calcitonin gene-related peptide family
RT peptide acting through the calcitonin receptor-like receptor/receptor
RT activity-modifying protein receptor complexes.";
RL J. Biol. Chem. 279:7264-7274(2004).
CC -!- FUNCTION: IMDL and IMDS may play a role as physiological
CC regulators of gastrointestinal, cardiovascular bioactivities
CC mediated by the CALCRL/RAMPs receptor complexes. Activates the
CC CAMP-dependent pathway.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expression was restricted to the intermediate
CC and anterior lobes of the pituitary.
CC -!- SIMILARITY: Belongs to the adrenomedullin family.
CC
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CC
CC EMBL; AB121036; BAD07413.1; -.
CC Amidation; Cleavage on pair of basic residues; Hormone; Signal.
CC SIGNAL 1 25
CC FT PROPEP 26 96 By similarity.
CC FT PEPTIDE 99 145 Adrenomedullin 2 (By similarity).
CC FT PEPTIDE 106 145 Intermedin-short (Potential).
CC FT DISULFID 108 113 By similarity.
CC FT MOD_RES 145 145 Tyrosine amide (G-146 provides amide
CC group) (Probable).
CC SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;

Query Match 56.8%; Score 451; DB 1; Length 146;
Best Local Similarity 65.3%; Pred. No. 1.4e-26;
Matches 94; Conservative 13; Mismatches 31; Indels 6; Gaps 4;

KW Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 96 By similarity.
FT PEPTIDE 99 145 Adrenomedullin 2 (By similarity).
FT PEPTIDE 106 145 Intermedin-short (Potential).
FT DISULFID 108 113 By similarity.
FT MOD_RES 145 145 Tyrosine amide (G-146 provides amide
FT group) (Probable).
FT SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;

Query Match 56.8%; Score 451; DB 1; Length 146;
Best Local Similarity 65.3%; Pred. No. 1.4e-26;
Matches 94; Conservative 13; Mismatches 31; Indels 6; Gaps 4;

QY 6 TAAAGCISILCLQPGSLRSRSGDPRPVKPREPPARSSSLOPHAPRPVWVKLHRA 65
Db 8 TWTFCISLLYL-LPGTLSSGLG---KGLRPREPPAKIPSSGPGHPSLRVWVKPPHA 63
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QY 66 LOAQ-RGAGLAPVMGQPLRDGGRQHSRPRRTQAQLLRVGCVLGTCCVQNLSHRL 124
Db 64 LQPQGRGNPALATVHLP-QGGSGSRHPGQRTGTSRRPAPHAQLLRVGCVLGTCCVQNLSHRL 122

QY 125 WOLMGPAQRDSAPVDPSPSPHSYG 148
Db 123 WOLVPSGRDSDAPVDPSPSPHSYG 146

RESULT 4
AAT01302 PRELIMINARY; PRT; 146 AA.
AC AAT01302;
DT 10-MAY-2004 (TReMBLrel. 27, Created)
DT 10-MAY-2004 (TReMBLrel. 27, Last sequence update)
DE Adrenomedullin 2 precursor (Intermedin) [Contains: Adrenomedullin 2
DE (Intermedin-long) (IMDL); Intermedin-short (IMDS)].
GN Name=Adm2; Synonyms=Am2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Chang C.L., Roh J., Hsu S.Y.;
RT "Rat IMD sequence.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY590103; AAT01302.1; -.
SQ SEQUENCE 146 AA; 15572 MW; C87043237AD29DDC CRC64;

Query Match 56.8%; Score 451; DB 2; Length 146;
Best Local Similarity 65.3%; Pred. No. 1.4e-26;
Matches 94; Conservative 13; Mismatches 31; Indels 6; Gaps 4;

QY 6 TAAAGCISILCLQPGSLRSRSGDPRPVKPREPPARSSSLOPHAPRPVWVKLHRA 65
Db 8 TWTFCISLLYL-LPGTLSSGLG---KGLRPREPPAKIPSSGPGHPSLRVWVKPPHA 63

QY 66 LOAQ-RGAGLAPVMGQPLRDGGRQHSRPRRTQAQLLRVGCVLGTCCVQNLSHRL 124
Db 64 LQPQGRGNPALATVHLP-QGGSGSRHPGQRTGTSRRPAPHAQLLRVGCVLGTCCVQNLSHRL 122

QY 125 WOLMGPAQRDSAPVDPSPSPHSYG 148
Db 123 WOLVPSGRDSDAPVDPSPSPHSYG 146

RESULT 5
Q75XW7 PRELIMINARY; PRT; 168 AA.
AC Q75XW7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Adrenomedullin-2.
GN Name=ADM2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphii; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost
RT fish.";
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMBL; AB120296; BAD02342.1; -.
SQ SEQUENCE 168 AA; 18544 MW; A5905E7CC112669B CRC64;
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OX NCB1_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost
RT fish.";
RL Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR EMEL; AB120297; BAD02343.1; -
SQ SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;

Query Match 25.7%; Score 204; DB 2; Length 159;
Best Local Similarity 34.8%; Pred. No. 5.8e-08;
Matches 62; Conservative 16; Mismatches 32; Indels 68; Gaps 9;

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Db      10  CISESLFLRLETPAELEPDENDENLDDIIIDORRDKSVSRQKNDIVPPL-----A 59
Qy      46  SSIQPR-----HPAPRPVVWKL-----HRAQLAQRGAGLAPYMGQPLRDGGRQHS- 90
Db      60  SLSLSPKWLKSHSGIHSGVKVWLSLAWARPORLFRARR-----HIHSR 103
Qy      91  GPRHSGPRTOQLLRVGVCLGTCOVNLSHRLWLMGPAGRQDSAPVDPSPSPHSYG 148
Db      104  GMRGHHYPHPN--QLIRAGCALGTCOVNLSHRLYQLIGOSGRDDSSPINPKPSHSYG 159

RESULT 8
BAD02343
ID      BAD02343      PRELIMINARY;      PRT;      159 AA.
AC      BAD02343;
DT      14-APR-2004 (TtEMBLrel. 27, Created)
DT      14-APR-2004 (TtEMBLrel. 27, Last sequence update)
DT      14-APR-2004 (TtEMBLrel. 27, Last annotation update)
DE      Adrenomedullin-3.
GN      ADM3.
OS      Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;

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OC
CX
NN
RP
RX
RA
RY
RT
RL
RL
DR
SQ

NCBI_TaxId=31033;
[1]
SEQUENCE FROM N.A.
MEDLINE=22984567; PubMed=14623291;
Ogoshi M., Inoue K., Takei Y.;
"Identification of a novel adrenomedullin gene family in teleost
fish.";
Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
ENBL: AB120297; BAD02343.1; -.
SEQUENCE 159 AA; 18028 MW; F1863B20100E254D CRC64;

Query Match 25.7%; Score 204; DB 2; Length 159;
Best Local Similarity 34.8%; Pred. No. 5.8e-08;
Matches 62; Conservative 16; Mismatches 32; Indels 68; Gaps 9;

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Db      10  C I S L L S F L R L E T T L P A E E L P D E N R L D D I I D Q R D K S V S R S Q K N I D V P P L -----A 59
Qy      46  S S I O P R -----H P A P P V W K L -----H R A L Q A R C A G L A P V M G Q P L R D G G R Q H S - 90
Db      60  S S L S P K W L S K H G I H S G V K V L F S L A W A R P Q R L F R A R -----H I H S R 103
Qy      91  G P R H S G P R T Q A L L R V C V L G T C V Q N L S H R L W O L M G P A G R Q D S A P V D P S P H S Y G 148
Db     104  G M R G H Y P H P N --Q L I R A G C A L G T C V Q N L S H R L Y Q L I Q S G R D D S S P I N K S P H S Y G 159

RESULT 9
Q61FS9
ID  Q61FS9      PRELIMINARY;      PRT;      140 AA.

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[illegible]

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RT clone:P0483C08.1;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004837; BAD21873.1; -.
KW Transferase.
SQ SEQUENCE 953 AA; 107236 MW; DECC9A24EACF78EA CRC64;

Query Match
Best Local Similarity 12.4%; Score 98.5; DB 2; Length 953;
Matches 43; Conservative 16; Mismatches 53; Indels 51; Gaps 8;

QY 22 SLRSLSGGDPRPVKPREPP-----ARSPSSSLOP----- 50
DB 3 SLOQCGGDRPQPOAAPALLGGADWLGFGRAAAEIDSVASPSAFLLPPAPPVDARA 62

QY 51 -RHAPAPPVVVKLHRAQAQAGAGLAPVMGQPLRDG---GROHSGPRHSGPRRTQAO 105
DB 63 QAQPEKPP---KQLGAVDVERHLALA---HQNYSRGYKEALEHGNIVYEKNPRTD-NL 115

QY 106 LRVCVLGTCQVQNLSHRLWQMGAPGRQDSAPVDPSPSHSYG 148
DB 116 LLLGAIY--YQIRNYD-----MCIKNEEALAIIDFNFAECYG 150

RESULT 13
BAD21878
ID BAD21878 PRELIMINARY; PRT; 953 AA.
AC BAD21878;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative O-linked N-acetyl glucosamine transferase.
GN OSUNBA0048K16.5.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
CX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
clone:OSUNBA0048K16.5."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004864; BAD21878.1; -.
KW Transferase.
SQ SEQUENCE 953 AA; 107236 MW; DECC9A24EACF78EA CRC64;

Query Match
Best Local Similarity 12.4%; Score 98.5; DB 2; Length 953;
Matches 43; Conservative 16; Mismatches 53; Indels 51; Gaps 8;

QY 22 SLRSLSGGDPRPVKPREPP-----ARSPSSSLOP----- 50
DB 3 SLOQCGGDRPQPOAAPALLGGADWLGFGRAAAEIDSVASPSAFLLPPAPPVDARA 62

QY 51 -RHAPAPPVVVKLHRAQAQAGAGLAPVMGQPLRDG---GROHSGPRHSGPRRTQAO 105
DB 63 QAQPEKPP---KQLGAVDVERHLALA---HQNYSRGYKEALEHGNIVYEKNPRTD-NL 115

QY 106 LRVCVLGTCQVQNLSHRLWQMGAPGRQDSAPVDPSPSHSYG 148
DB 116 LLLGAIY--YQIRNYD-----MCIKNEEALAIIDFNFAECYG 150

RESULT 14
Q75XW4
ID Q75XW4 PRELIMINARY; PRT; 123 AA.
AC Q75XW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Adrenomedullin-5.

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GN Name=ADMS;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
CX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost
fish.";
RL Biochem. Biophys. Res. Commun. 311:1072-1077 (2003).
DR EMBL; AB120299; BAD02345.1; -.
SQ SEQUENCE 123 AA; 13538 MW; D3ED4CDBCFC4ECEB CRC64;

Query Match
Best Local Similarity 12.3%; Score 98; DB 2; Length 123;
Matches 36; Conservative 10; Mismatches 33; Indels 46; Gaps 6;

QY 50 PRHPAPRPVV-----WKLHRAQAQAGAGLAPV-----MGQPLR 83
DB 18 PLRPTPRPDVLPAGTVQSGSLKTETQAOHAQALRIVPFISEIKNLNLEILKHMAARLR 77

QY 84 DGRQHSGRPRHSGPRRTQAOQLLRVGCVLGTCQVQNLSHRLWQMGAPGRQDSAPVDPSS 143
DB 78 -----PRR--APQR-----GCQVGTQVHNLANKLYQIGRQGDSTKV--ND 117

QY 144 PHSYG 148
DB 118 PQGYG 122

RESULT 15
BAD02345
ID BAD02345 PRELIMINARY; PRT; 123 AA.
AC BAD02345;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Adrenomedullin-5.
GN ADMS.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Takifugu.
CX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22984567; PubMed=14623291;
RA Ogoshi M., Inoue K., Takei Y.;
RT "Identification of a novel adrenomedullin gene family in teleost
fish.";
RL Biochem. Biophys. Res. Commun. 311:1072-1077 (2003).
DR EMBL; AB120299; BAD02345.1; -.
SQ SEQUENCE 123 AA; 13538 MW; D3ED4CDBCFC4ECEB CRC64;

Query Match
Best Local Similarity 12.3%; Score 98; DB 2; Length 123;
Matches 36; Conservative 10; Mismatches 33; Indels 46; Gaps 6;

QY 50 PRHPAPRPVV-----WKLHRAQAQAGAGLAPV-----MGQPLR 83
DB 18 PLRPTPRPDVLPAGTVQSGSLKTETQAOHAQALRIVPFISEIKNLNLEILKHMAARLR 77

QY 84 DGRQHSGRPRHSGPRRTQAOQLLRVGCVLGTCQVQNLSHRLWQMGAPGRQDSAPVDPSS 143
DB 78 -----PRR--APQR-----GCQVGTQVHNLANKLYQIGRQGDSTKV--ND 117

QY 144 PHSYG 148
DB 118 PQGYG 122

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Db 118 PQYG 122

Search completed: October 22, 2004, 08:54:32
Job time : 201 secs

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OM protein - protein search, using sw model

Run on: October 22, 2004, 08:46:21 ; Search time 40 Seconds
(without alignments)
245.377 Million cell updates/sec

Title: US-10-723-368-2

Perfect score: 794

Sequence: 1 MARIPTAALGICISLLCLQLP.....GPAGRODSAPVDPSPSHYS 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	110	13.9	379	4	US-09-252-991A-26924	Sequence 26924, A
2	108	13.6	362	4	US-09-252-991A-31641	Sequence 31641, A
3	107.5	13.5	514	4	US-09-252-991A-28208	Sequence 28208, A
4	103.5	13.0	621	4	US-09-252-991A-30689	Sequence 30689, A
5	103	13.0	142	4	US-09-252-991A-21581	Sequence 21581, A
6	102.5	12.9	417	4	US-09-252-991A-24041	Sequence 24041, A
7	101	12.7	327	4	US-09-252-991A-30948	Sequence 30948, A
8	100.5	12.7	528	4	US-09-252-991A-18286	Sequence 18286, A
9	100	12.6	464	4	US-09-252-991A-25833	Sequence 25833, A
10	100	12.6	783	4	US-09-252-991A-18035	Sequence 18035, A
11	99.5	12.5	763	4	US-09-252-991A-30146	Sequence 30146, A
12	99	12.5	373	4	US-09-252-991A-21973	Sequence 21973, A
13	99	12.5	588	4	US-09-252-991A-30690	Sequence 30690, A
14	98.5	12.4	176	4	US-09-252-991A-30542	Sequence 30542, A
15	98.5	12.4	275	4	US-09-252-991A-23976	Sequence 23976, A
16	98.5	12.4	362	4	US-09-252-991A-31016	Sequence 31016, A
17	98.5	12.4	364	4	US-09-252-991A-19923	Sequence 19923, A
18	98.5	12.4	498	4	US-09-252-991A-21973	Sequence 21973, A
19	98.5	12.4	642	4	US-09-252-991A-24767	Sequence 24767, A
20	98.5	12.4	642	4	US-09-252-991A-32104	Sequence 32104, A
21	98	12.3	266	4	US-09-252-991A-30538	Sequence 30538, A
22	97.5	12.3	142	4	US-09-252-991A-16714	Sequence 16714, A
23	97.5	12.3	416	4	US-09-252-991A-24575	Sequence 24575, A
24	97.5	12.3	436	4	US-09-252-991A-31117	Sequence 31117, A
25	97	12.2	317	4	US-09-252-991A-31126	Sequence 31126, A
26	97	12.2	653	4	US-09-252-991A-21418	Sequence 21418, A
27	97	12.2	720	4	US-09-252-991A-31915	Sequence 31915, A

28	96.5	12.2	230	4	US-09-252-991A-28838	Sequence 28838, A
29	96.5	12.2	392	4	US-09-252-991A-31291	Sequence 31291, A
30	96.5	12.2	538	4	US-09-252-991A-21622	Sequence 21622, A
31	96	12.1	260	4	US-09-252-991A-31985	Sequence 31985, A
32	95.5	12.0	315	4	US-09-252-991A-20553	Sequence 20553, A
33	95.5	12.0	457	4	US-09-252-991A-29671	Sequence 29671, A
34	95	12.0	1228	4	US-09-252-991A-17764	Sequence 17764, A
35	94.5	11.9	225	4	US-09-252-991A-25503	Sequence 25503, A
36	94.5	11.9	372	4	US-09-252-991A-23226	Sequence 23226, A
37	94.5	11.9	404	4	US-09-252-991A-21555	Sequence 21555, A
38	94.5	11.9	414	4	US-09-252-991A-27895	Sequence 27895, A
39	94.5	11.9	626	4	US-09-252-991A-27835	Sequence 27835, A
40	94.5	11.9	770	4	US-09-252-991A-28510	Sequence 28510, A
41	94	11.8	193	4	US-09-252-991A-19226	Sequence 19226, A
42	94	11.8	246	4	US-09-252-991A-20289	Sequence 20289, A
43	94	11.8	416	4	US-09-252-991A-17590	Sequence 17590, A
44	94	11.8	489	4	US-09-252-991A-16940	Sequence 16940, A
45	94	11.8	531	4	US-09-252-991A-24404	Sequence 24404, A

ALIGNMENTS

RESULT 1
US-09-252-991A-26924
; Sequence 26924, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26924
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26924

Query Match Similarity 13.9%; Score 110; DB 4; Length 379;
Best Local Similarity 29.2%; Pred. No. 0.0026;
Matches 50; Conservative 15; Mismatches 56; Indels 50; Gaps 8;
QY 4 IPTAALGICISLLC-----LQLFGSLRSLSGGDF-----RFVKPREPPARSPS 45
Db 70 LPHVGLGRRPLLVAVGHRPADRHVRHLQLQGTAVRRLQHGFAPFDPRAVRTQHPGAARPA 129
QY 46 SSL-----OPHPAPFPVWKLHRLAQORAGLAPVWQPLRDGGRHSGRRHSG 97
Db 130 RLVRLLGREGQPDALRLLSAEYHRP-FATTGHHGIIQ-----ROERAPGRHAG 177
QY 98 PRRTQAQLLRGCVLGTGCOVNLSHRLWQLMGPAGRODSAPVDPSPSHYSYG 148
Db 178 HQHRAG-----DLGCRLOQPA-RLPSVAAP-----RHPVDFGLHRPG 216

RESULT 2
US-09-252-991A-31641
; Sequence 31641, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18

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; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31641
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31641

Query Match
Best Local Similarity 13.6%; Score 108; DB 4; Length 362;
Matches 50; Conservative 16; Mismatches 42; Indels 44; Gaps 10;

QY 17 LQLPGSLSRS--LGGDPRVVKP-----REP---PARSPSS- 47
Db 206 LRLRLNLTARRCAGGLFRPAGGQMAARPGRGAPQADWRRAPRCGPRTFVAAR 265

QY 48 --LQPRHPAPRVVWKLHRLAQRGAGLAPVMGQPLRDGGRGHSGPRRHSGPRRTQAOL 105
Db 266 RDLRPEVGAPRPAIRRRER--RADHGATAA---GGVAGEGQRPASGPRQ---PRRARAQR 317

QY 106 LRVCGLVGTQCVQNLHRLWQLMGAPGRQDSA 137
Db 318 ROAGQV-GKDGQCPQSR--LRGP-GRAPGA 344

RESULT 3
US-09-252-991A-28208
; Sequence 28208, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28208
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28208

Query Match
Best Local Similarity 13.5%; Score 107.5; DB 4; Length 514;
Matches 54; Conservative 11; Mismatches 51; Indels 79; Gaps 11;

QY 20 PGSLSRSL-----GGDPR---PVKPREPPARS-----PSSSLOP-- 50
Db 178 PGRFRRALPARLOQTABDRGKGAAPAGADPRAYFGFPQPPWRCRALPGGSLRPAG 237

QY 51 -RHAPAPRVVWKLHRLAQRGAGLAPVMGQ-----PLRDGGRGH-----SGPR 93
Db 238 EHHQRP-----CRRAPCORPGRVLPAGGQAVHPAARTRTPRLRAGGRHWELOPAG 290

QY 94 RHSGPRRTQALLRVGCVLTG-----CQVONLSHRLWQ-----LMGPAG 132
Db 291 AAVRPGRLARALPAGALGAGPVFAAPGAPGCGRRGLSPRLLOPAGFRPGLQG-AL 349

QY 133 RQDSA-----PVDPS 143
Db 350 RDDAERGAWPLDPTT 364

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RESULT 4
US-09-252-991A-30689

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; Sequence 30689, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30689
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30689

Query Match
Best Local Similarity 13.0%; Score 103.5; DB 4; Length 621;
Matches 40; Conservative 13; Mismatches 45; Indels 43; Gaps 7;

QY 31 PRVVKPREPPARSPSSSLQPRHPAPRVVWKLHRLAQRGAGLAPVMGQPLRDGGR--- 87
Db 421 FDPARTQPP-RQWLLAVAFGQRPAPV-----ESRPAHRQPALAP--GRPIRRAGALAY 472

QY 88 --QHSGRHSGPRRTQAQLRVGCVLTGCVQNL--SHELWOL----- 127
Db 473 PGEHGAARRHADPR-----GTAAQORLAAASRALRQHASARPAAGNRRRAGD 520

QY 128 MGPAQRQDSAPVDFSPHSYSG 148
Db 521 LPPAGRHRHVHAAAPAPRATG 541

RESULT 5
US-09-252-991A-21581
; Sequence 21581, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21581
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21581

Query Match
Best Local Similarity 13.0%; Score 103; DB 4; Length 142;
Matches 35; Conservative 6; Mismatches 34; Indels 14; Gaps 7;

QY 25 RSLGGDP---RPVKPREPPARSPSSSLQPRH--PAP-RPVVWKLHRLAQOR-GAGLAP 76
Db 11 RTRGGQPAQRRALQPRRP---PGGACQORRLPAPRPRPWARRRRRTAGAVGVLP 67

QY 77 VMGQPLRDGGRGHSG---PRHSGPRRTQA 103
Db 68 -RTQPEQFGTRPGEGHPRPRRAPRA 95

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RESULT 6

US-09-252-991A-24041
 ; Sequence 24041, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24041
 ; LENGTH: 417
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24041

Query Match 12.9%; Score 102.5; DB 4; Length 417;
 Best Local Similarity 27.9%; Pred. No. 0.017;
 Matches 36; Conservative 8; Mismatches 58; Indels 27; Gaps 3;
 QY 20 PGS-LRSLSGDRPVKPREPPARSPSSSQPRHPAPRVVVKLHRLAQAGAGLAFVM 78
 DB 216 PGSGTHRALVGDHPHPPAGSRADAAPPQORAAAPHPVPCFARRRLSTGGGKPGRRPFGI 275
 QY 79 -----GQPLRDGGEQHSGRHSGPRRTQALLRVGCVLTGTCQVONLSHRLWQMGPA 132
 DB 276 PRSAPGPHVSRGPPDPGDRRLHPRR-----AHQORRRRAPP 315
 QY 133 RQDSAPVDP 141
 DB 316 PGRLLVYRP 324

RESULT 7
 US-09-252-991A-30948
 ; Sequence 30948, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 30948
 ; LENGTH: 327
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30948

Query Match 12.7%; Score 101; DB 4; Length 327;
 Best Local Similarity 30.2%; Pred. No. 0.018;
 Matches 54; Conservative 15; Mismatches 59; Indels 52; Gaps 11;
 QY 11 CISLLCLQLPGSLRSLSGDRPVK-----PREPPARSPSS----- 46
 DB 55 CLPLRLRTGTAGRQPGDGPAAKVAAGRGRPVAVLCARPLAPGRAPGADRRGR 114
 QY 47 ----SLOPRHPA----PRPVVVKLHRA-LQAGAGLA--PVMGQPLRDGGRQHSQ--PR 93
 DB 115 GRALSRRQPRRAAGQOPEP-----HRAGLRARRRAGLACPATSRRLAAGRGVHGLHPA 169
 QY 94 RHSG-----PRRTQALLRVGCVLTGTCQVONLSHRLWQMGPAQRQDSAPVD---PSSP 144

DB 170 VEPGLYQPTRIDRAALVRQVLRPCZARLRPRRTAAVAG-AGRA-ARPDGQWPGAP 226
 RESULT 8
 US-09-252-991A-18286
 ; Sequence 18286, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18286
 ; LENGTH: 528
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18286

Query Match 12.7%; Score 100.5; DB 4; Length 528;
 Best Local Similarity 28.0%; Pred. No. 0.036;
 Matches 47; Conservative 9; Mismatches 43; Indels 69; Gaps 9;
 QY 28 GGDPRPVK-----REPPARSPSSSQ-----PRHPAPRVVVKLHRL 66
 DB 52 GDDPVAADPRRGAMLPAGHPAGGADLRQPAALPGLALHLRVPRHPAVHPVAVLLHRL 111
 QY 67 QAO-----RGAGLAPVMQPIR--DGG-----RQHSGRPRISGPRPT 101
 DB 112 QPECHTRPGLSQRVLPRLRLQHLGAGLRP---QHLRLHDGNLRDRDQEHAPRRSGSGLRL 168
 QY 102 QAO-----LRVGCVLGTQCVONLS-----HRLWQMGPA 131
 DB 169 HGRLLPLPAHRPALGAAPGTAVLQORSDPDAAFHLLGVHR--HSAGPA 214

RESULT 9
 US-09-252-991A-25833
 ; Sequence 25833, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25833
 ; LENGTH: 464
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25833

Query Match 12.6%; Score 100; DB 4; Length 464;
 Best Local Similarity 28.4%; Pred. No. 0.035;
 Matches 42; Conservative 13; Mismatches 47; Indels 46; Gaps 9;
 QY 29 GDP-RPVK-----PREPPARSPSSSQPRHPA-----PRPVVVKLHRLAQAGRA 72
 DB 185 GDHPRGRRVPGPADAPARAGRGDQPRQGDHGHGAAVAGHPAPAVLIRHLSQRHRGP 244

QY 73 GLAPVNGQFLR-----DGRQHSGRHSGRRTQAQLLRVGVGLTCOVNLS 121
 Db 245 ARGF--RRPVQRAGADAPADPGRH---RRGNGLRR--RQLPR-----PVEGTD 290

QY 122 HRLW-----QLMGAPAGQDSAPVDPSP 144
 Db 291 RRAWPGRRHLEPEPGRRGHYPHPP 318

RESULT 10
 US-09-252-991A-18035
 ; Sequence 18035, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18035
 ; LENGTH: 783
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-18035

Query Match 12.6%; Score 100; DB 4; Length 783;
 Best Local Similarity 27.2%; Pred. No. 0.064;
 Matches 44; Conservative 12; Mismatches 56; Indels 50; Gaps 7;

QY 19 LPSLSRSLGSDPRPVKPREPPA---RSPSSSLQPRHPAPRPVVKLHRLAQORGAGLA 75
 Db 3 LPTAFPRSGADRPQTEPARPPAAGRRVPAAGLGRGAVQPRP-----AGLR 48

QY 76 PVNGQPLRDGGRHSGRPR---HSGPRTQAQLLRVG-----CVLGT--CQVQLSH 122
 Db 49 PCI---LHPOGQADPLRAVPAERPARTGLARRAGKGAREDLAVRGTRLPVDRRYR 105

QY 123 RLWQLMGPA-----GRQDSAPVDPSPSHY 147
 Db 106 RAGRRRPAFLRGIEGKTRRRRVRQRTQASARPSPHRY 147

RESULT 11
 US-09-252-991A-30146
 ; Sequence 30146, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 30146
 ; LENGTH: 763
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-30146

Query Match 12.5%; Score 99.5; DB 4; Length 763;
 Best Local Similarity 25.7%; Pred. No. 0.07;
 Matches 55; Conservative 12; Mismatches 72; Indels 75; Gaps 8;

QY 3 RIFTAALGCISLCLQLPGSLRSLSG-----GDRPV-----KPREPPARS 43
 Db 10 RRPVAP--GLVAALPAAWPTARRRRTGRRHAAGARSAPVAPGGPRVAPRRHRRPGHPFAVA 68

QY 44 PSSSLQPRHPA-----PRPVVKLHRLAQORGAGLAPVNGQPLRDGGRHSGRHRSGP 98
 Db 69 PDRSLPAAGFAAARRRPRGAGGQRR--RARRGAGTAERRRKPEDDAAGRAGSAVORHGL 126

QY 99 RR-----TQAQLL-----RVGCVLGTCCOVNLS 121
 Db 127 RQVPLPAGRAGRLRQRLARTLVLRQAALAFRRCHRRGVGQRPGGRLGTVRHAGLR 186

QY 122 HR-----LWQLMGAPAGQDSAPVDPSP 144
 Db 187 PRGAQGRVHPVDPVRQRRGPGDRPRRCPADHARP 220

RESULT 12
 US-09-252-991A-24961
 ; Sequence 24961, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24961
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-24961

Query Match 12.5%; Score 99; DB 4; Length 373;
 Best Local Similarity 31.4%; Pred. No. 0.034;
 Matches 44; Conservative 10; Mismatches 46; Indels 40; Gaps 8;

QY 24 SRSLGSDPRPVKPREPPARSFSSSLQPRHPA---PRPVVKLHRLAQORGAGLAPVNGQ 81
 Db 93 ARLRGAVPREARP--PPGARRSGRTHPRPLAEDARPL-----AGHADPGHGTAPHRAYP 144

QY 82 LRDCGRHSGS-----GPRRH--SGPRR-----TQAQLLRVGVGLTCOVNLSHR 123
 Db 145 ASPPGRRGQQLPPVARRGAFGPRRAAGHRDSFGDRRAPRLRRGVQLQPC-LQALE-- 201

QY 124 LWQLMGAPAGQDSAPVDPSP 143
 Db 202 -----RHDAPVSPAA 212

RESULT 13
 US-09-252-991A-30690
 ; Sequence 30690, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

```

; SEQ ID NO 30690
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30690

Query Match      12.5%; Score 99; DB 4; Length 588;
Best Local Similarity 28.9%; Pred. No. 0.058;
Matches 48; Conservative 10; Mismatches 46; Indels 62; Gaps 9;

QY 21 GSLRSLSGDP-RPVKP-----REPPARSPSSSLQPRHP-----A 54
Db 266 GADGRELIGNPAAPRRPGILLAHPOPAARGRRRPAARQPTALAPRRPLALVRHPRAGLQ 325
QY 55 PRPVVVKLHRAALQAQRGAGLAPVMQOPLRDGGRQHSPPR-----HSG-----PRR 100
Db 326 PRP-----QRSGAPDRRGQGHLLHRRGEQPAARERPLPHAGKHQHRDILLHRRR 376
QY 101 TQQLLRVGCVLGTCCQVQNLHRLWQLMG-----PAGRQDSAPVDP 141
Db 377 TQQLRQ---PLGTARV-----RLQPGMGAAQRPPSDRHQPAPARP 414

RESULT 14
US-09-252-991A-30542
; Sequence 30542, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30542
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30542

Query Match      12.4%; Score 98.5; DB 4; Length 176;
Best Local Similarity 31.8%; Pred. No. 0.016; 50; Indels 45; Gaps 8;
Matches 47; Conservative 6; Mismatches 50; Indels 45; Gaps 8;

QY 31 PRPVKPREPPARSPSSSLQPRHPAP--RPVVKLHRAALQAQRGAGLA-----75
Db 40 PRPVL---PARQGPRESQQHPAPPLRPG---HARRAARILLAAQAQRRAAAGGPAGR 91
QY 76 -----PVMGQPLRDGGRQHSPP-----RRHSGPRRTQAQLRV-----GCVLGTCCV 117
Db 92 RLHRPRRQOPLR---RQQLPAAARRGPGRTNRQALRQAQSRPQFGGATGRPQR 148
QY 118 QNLHRLWQLMGAG-RQDSAPVDPSSP 144
Db 149 RRLCRRGRLEAAGRPALLPADGPR 176

RESULT 15
US-09-252-991A-23976
; Sequence 23976, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

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; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23976
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23976

Query Match      12.4%; Score 98.5; DB 4; Length 275;
Best Local Similarity 26.9%; Pred. No. 0.027;
Matches 45; Conservative 16; Mismatches 53; Indels 53; Gaps 8;

QY 16 CLQLPGSLRSLSGG--DERPVKPRE--PPAESPSSSSLQPRHPAPRPVVKLHRAALQAQRG 71
Db 11 CORAAGAADRRRGQRLDPRQSRPRRHADSVTPVQGGKPAQP-----VORRG 58
QY 72 -----AGLAPVMGQPLRDGGRQHSPPRRHSGPRR-----TQQL-LRV 108
Db 59 LRPPGPRGDAGIAARLGVLRERRGARRHYRPRQWRARRGKMGVPVQQLDETQALRLDS 118
QY 109 GCVLGTCCVQ-----NLSHRLWQLMGAPAGRQDSAPVDPSSP 144
Db 119 QQLAGSRGTQLRDPGRPPQRTTRRAVRLQHSAGPAG---AAPAHPTP 162

Search completed: October 22, 2004, 08:55:57
Job time : 42 secs

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61 KLHRALOAORGAGLA PVMGQPLRDGGROHSGPRRHSGPRRTOAOLLRVGCVLGTQOVNL 120

Db	61	KLHRLAQAGAGLAPVNGQPLRDGGRCHSGPRHSGSPRRQTQALLKVGCVLGTQVQNL	120
Qy	121	SHRLWLMGPAGRODSAPVDPSSPHSYG	148
Db	121	SHRLWLMGPAGRODSAPVDPSSPHSYG	148

```

RESULT 2
US-10-723-368-5
; Sequence 5, Application US/10723368
; Publication No. US20040204353A1
; GENERAL INFORMATION:
; APPLICANT: Sheau Yu Teddy Hsu
; TITLE OF INVENTION: Intermedin and Its Uses
; FILE REFERENCE: STAN-284
; CURRENT APPLICATION NUMBER: US/10/723,368
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,327
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 47
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-723-368-5

```

```

RESULT 3
US-10-437-963-202661
; Sequence 202661, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 202661
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(311)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_9791C.1.pep
US-10-437-963-202661

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[illegible]

```

RESULT 4
US-10-425-114-56462
; Sequence 56462, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56462
; LENGTH: 386
; TYPE: ERT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73224A12_F11.pep
US-10-425-114-56462

```

RESULT 5
US-10-437-963-109275
; Sequence 109275, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966


```
; SEQ ID NO 109275
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13448C.1.pep
US-10-437-963-109275
```

```
Query Match 13.2%; Score 105; DB 16; Length 413;
Best Local Similarity 28.8%; Pred. No. 1.3;
Matches 57; Conservative 15; Mismatches 52; Indels 74; Gaps 12;
```

```
Qy 3 RIPTAALGICSLCLQLPGSLRSL---GGDPKPVKPREPPARSPSSSLQPRH----- 52
Db 6 RLAGAALGCLSLFL-----LSRALLFSQDDPEPVK---RPDEASSISLPDRIATIAAAA 56
Qy 53 PAPRPVVKLHRAQAQAGAGAPVM-----GQPLEDGG----- 87
Db 57 PAPSP-----ATAASDGSFAPAQDEVRCDLFDGSWVYPAGYPLVDAGECPFLSDQV 109
Qy 88 --QHSGRPRHSG-----PRTQAQL-LRVGCVLTGTCVQ-----NLSHRLWQ----- 126
Db 110 TCRENG-RPDSGYEHWKQPRCAALELRGEMLEQCRDKRVVLVGDLSLNWWSLAC 168
Qy 127 -LMGPAGQDSAPVDPS 143
Db 169 ILVAAAPDRSRATVDDAS 186
```

```
RESULT 6
US-10-425-114-64514
; Sequence 64514, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64514
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-032-G9_FLI.pep
US-10-425-114-64514
```

```
Query Match 13.0%; Score 103; DB 15; Length 556;
Best Local Similarity 28.0%; Pred. No. 2.5;
Matches 44; Conservative 18; Mismatches 45; Indels 50; Gaps 7;
```

```
Qy 17 LQLPGSLR--SLGDDRPVKPREPPARSPSSSLQPRHPAPRPVVKLHRAQAQRG--- 71
Db 53 LRLPQAQRPPQAVHGDGR---ORDPAQAAAGAHRLPL-PPPR-----HRLHRRGDLR 102
Qy 72 -----AGLAPVMGQPLRDGGRHSGPRHSGPRRTQAQLLRVGCVLGTGCV 117
Db 103 PAQHPGPRGLAHAGRGDRGLRLRCHRRALRDRPAPRGARLQRLHALPGAVAV 162
Qy 118 QNLSHRLWQLMGPAGRQDSAPVDPS-----SPHSYG 148
Db 163 V-----QDRALPARGGGVQPHGHG 184
```

```
RESULT 7
US-10-767-701-35404
```

```
; Sequence 35404, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53335)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 35404
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(179)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C66925_1.pep
US-10-767-701-35404
```

```
Query Match 12.8%; Score 101.5; DB 16; Length 179;
Best Local Similarity 32.2%; Pred. No. 1.1;
Matches 39; Conservative 4; Mismatches 41; Indels 37; Gaps 6;
```

```
Qy 31 PRPVKPREPPARSPSSSLQPRHPAPRPVVKLHRAQAQAGLAPVMGQPLRDGGRHS 90
Db 80 PRPAPRRRPPPPXPPRA-PFSPAPPAPPA-----APRGEGPAP-----PRARGGARRH 126
Qy 91 GPRRHS-----GPRRTQAQLLRVGCVLGTGCVQNLSHRLWQLMGPAGRQDSAPVDPS 143
Db 127 VPRRAARAAPAGQPRRLPAQRCRG-----RRLGAAGGGGRGP--PRS 169
Qy 144 P 144
Db 170 P 170
```

```
RESULT 8
US-10-450-436-28
; Sequence 28, Application US/10450436
; Publication No. US20040077832A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jian
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: JFY1 induces rapid apoptosis
; FILE REFERENCE: 01107.00062
; CURRENT APPLICATION NUMBER: US/10/450,436
; CURRENT FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-436-28
```

```
Query Match 12.7%; Score 101; DB 15; Length 242;
Best Local Similarity 29.7%; Pred. No. 1.6;
Matches 43; Conservative 9; Mismatches 57; Indels 36; Gaps 7;
```

```
Qy 18 QLPGLSRSLGGDPRPVKPREPPARSPSS-----SLOPR--HPAPRPVVKLH 63
Db 24 QLPGARR-----GFPRRPAPLPAPPGALGSLRLPLRPFRCPRRPHPAARCLPLRPH 78
Qy 64 RALQAQAGLAPVMGQPLRDGGRHSGPRHSGPRRTQAQLLRVGCVLGTGCVQNLSHR 123
Db 79 RPTRRRRRP-----GFPPLAWGSPQ---PAPRPAGRSSALALAGGAAPGVARQRPQ-- 128
```

QY 124 LWQMGAGAGQDSAPVDPSPSPHSYG 148
 Db 129 -----GSGGR--SHPGGSGSPRG 146

RESULT 9

US-10-767-701-34727
 ; Sequence 34727, Application US/10767701
 ; Publication No. US20040172684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 ; FILE REFERENCE: 38-21(53535)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO 34727
 ; LENGTH: 203
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C53158_1.pep
 US-10-767-701-34727

Query Match 12.5%; Score 99.5; DB 16; Length 203;
 Best Local Similarity 30.4%; Pred. No. 1.8;
 Matches 41; Conservative 10; Mismatches 43; Indels 41; Gaps 8;
 QY 17 LQLP---PGSLRSLSGDDP-RPVKPREPPARSPSSLSQPRHPAPRPVVKLHRLAQA---Q 69
 Db 12 LQLSPQGRQPSRAGAPREVRRPGG-----PPRPPPRPAPPGAHPDCHGGCID 64
 QY 70 RGAGLAPVMGP-----LRDGGROHSGPRHSGPRR-----TQALLRVG 109
 Db 65 GGAGAAFPFRPRPRAGAPALPLRDG-----GPDGGGPRQPLLRKRTWNTTTSQAIVG 119
 QY 110 CVLGTQVQNLSHRL 124
 Db 120 A--NVCPISLDYEV 132

RESULT 10

US-10-084-846A-6
 ; Sequence 6, Application US/10084846A
 ; Publication No. US2004006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREFZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: Patent in Ver. 3.2
 ; SEQ ID NO 6
 ; LENGTH: 19662
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
 ; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
 US-10-084-846A-6

Query Match 12.5%; Score 99.5; DB 15; Length 19662;

Best Local Similarity 28.9%; Pred. No. 1.7e+02;
 Matches 41; Conservative 11; Mismatches 49; Indels 41; Gaps 7;
 QY 17 LQLP-----GSLRSLSGDDPRPVKPREPPAR-SPSSLSQPRHPAPRPVVKLHRLAQA 68
 Db 4413 MRLPSTVVKFPEGLSRA--GQPRARPSATGFRFAAPLRPSGPPRRRAVRSH----- 4465
 QY 69 QRGAGLAPVMGPQLRDGGRQSHGSRHSGPRRTQALLRVGCVLGTQVQNLSHRLWQLM 128
 Db 4466 ----ACAPARCPA--GGRSSARRPRAPCAAGARPRSG-----R 4501
 QY 129 GPAGRODSAPVD--PSSPHSYG 148
 Db 4502 APAVPGGSAPESRRPARPPSHG 4523

RESULT 11

US-10-437-963-192117
 ; Sequence 192117, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 192117
 ; LENGTH: 851
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_88372C.1.pep
 US-10-437-963-192117

Query Match 12.4%; Score 98.5; DB 16; Length 851;
 Best Local Similarity 26.4%; Pred. No. 9;
 Matches 43; Conservative 16; Mismatches 53; Indels 51; Gaps 8;
 QY 22 SLRSLSGDDPRPVKPREPP-----ARSPSSLSQP----- 50
 Db 3 SLQQGGGDDPRPQQPAAAPALLGGADWLGFGRAAAEDESVAASPASFLPPAPPVDARA 62
 QY 51 -RHPAPRPVVKLHRLAQAQRGAGLAPVMGQPLRDG---GROHSGPRHSGPRRTQOAL 105
 Db 63 QAOPEKP---KOLGAVDVERHLALA---HONVRSKYYKEALEHGNIVIEKNPRTD-NL 115
 QY 106 LRVGCVLGTQVQNLHRLWQLMGPAGRODSAPVDPSPSPHSYG 148
 Db 116 LLLGAIY--YQIRNYD-----MCIKNEALAIIDENFAECYG 150

RESULT 12

US-10-084-846A-3
 ; Sequence 3, Application US/10084846A
 ; Publication No. US2004006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREFZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

Query Match 12.4%; Score 98.5; DB 15; Length 19695;
Best Local Similarity 27.8%; Pred. No. 2.1e+02; Indels 63; Gaps 7;
Matches 40; Conservative 7; Mismatches 34; Indels 63; Gaps 7;
Qy 29 GDRPVK---PREPPARSPSS---LQPHPA--PRPVVK-----61
Db 6166 GDRPRGPDGQAGRPEDRLGRPHGDPGPAVARASAPPPGCVFRLLRRHG 6225
Qy 62 -----LHRAIQRGAGL-----APVMGQPLRDG-----GRHSGP---92
Db 6226 PCGPRTGAHRARPPRAGAGRNPFVGRGLPGGAPPRGRRAGRGGRPLGRAHPGPSAV 6285
Qy 93 -----RRHSGPRRTQAQLRVG 109
Db 6286 PAGPPGRRGRDPRGTGRRARAG 6309

RESULT 13
US-10-408-765A-2462
; Sequence 2462, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2462
; LENGTH: 2527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2462

Query Match 12.3%; Score 98; DB 16; Length 2527;
Best Local Similarity 31.9%; Pred. No. 29; Indels 18; Gaps 5;
Matches 37; Conservative 10; Mismatches 51; Indels 18; Gaps 5;
Qy 29 GDRPVKPREPPARSPSSLSQPRHPAPRPVVMKHLRAIQAGAGLAPVMGQPLRDGGRQ 88
Db 484 GAPEAPEPEPPADD-----SPAEPPEPRAVGTNLSLPR-----FAPVVTTPVKAESP 533
Qy 89 HSGPRRHSGPRRTQAQLRVGCVLTGTCQVQNLSHRL-----WOLMGPAQRQDSAPVD 140
Db 534 HGAPALSNGP-QTOAQLIQ---PLQALQTQLLPQALPPPPQLOPPSPQOMPPLLE 585

RESULT 14
US-10-408-765A-866
; Sequence 866, Application US/10408765A

; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 866
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-866

Query Match 12.3%; Score 98; DB 16; Length 2715;
Best Local Similarity 31.9%; Pred. No. 31; Indels 18; Gaps 5;
Matches 37; Conservative 10; Mismatches 51; Indels 18; Gaps 5;
Qy 29 GDRPVKPREPPARSPSSLSQPRHPAPRPVVMKHLRAIQAGAGLAPVMGQPLRDGGRQ 88
Db 672 GAPEAPEPEPPADD-----SPAEPPEPRAVGTNLSLPR-----FAPVVTTPVKAESP 721
Qy 89 HSGPRRHSGPRRTQAQLRVGCVLTGTCQVQNLSHRL-----WOLMGPAQRQDSAPVD 140
Db 722 HGAPALSNGP-QTOAQLIQ---PLQALQTQLLPQALPPPPQLOPPSPQOMPPLLE 773

RESULT 15
US-10-094-749-2528
; Sequence 2528, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2528
; LENGTH: 1003
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2528

Search completed: October 22, 2004, 09:06:05
Job time : 130 secs

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OM protein - protein search, using sw model

Run on: October 22, 2004, 08:37:31 ; Search time 154 Seconds
(without alignments)
344.753 Million cell updates/sec

Title: US-10-723-368-2

Perfect score: 794

Sequence: 1 MARIPTAALGICSLICLQLP.....GPAGRQDSAPVDPSPSPHSYG 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	794	100.0	148	8	ADO61520	Human int
2	254	32.0	47	8	ADO61523	Human int
3	110	13.9	379	7	ABO78178	Pseudomon
4	108	13.6	362	7	ABO82895	Pseudomon
5	107.5	13.5	514	7	ABO79462	Pseudomon
6	103.5	13.0	621	7	ABO81943	Pseudomon
7	103.5	13.0	1938	6	ABE98398	Streptomy
8	103	13.0	142	7	ABO72835	Pseudomon
9	102.5	12.9	417	7	ABO75295	Pseudomon
10	101	12.7	242	3	AAV96318	Mammalian
11	101	12.7	242	5	ABG32397	Human JFY
12	101	12.7	327	7	ABO82202	Pseudomon
13	100.5	12.7	528	7	ABO69540	Pseudomon
14	100	12.6	464	7	ABO77087	Pseudomon
15	100	12.6	555	4	ABG16571	Novel hum
16	100	12.6	783	7	ABO69289	Pseudomon
17	99.5	12.5	763	7	ABO81400	Pseudomon
18	99	12.5	373	7	ABO76215	Pseudomon
19	99	12.5	588	7	ABO81944	Pseudomon
20	98.5	12.4	176	7	ABO81796	Pseudomon
21	98.5	12.4	275	7	ABO75230	Pseudomon
22	98.5	12.4	307	4	ABG04221	Novel hum
23	98.5	12.4	362	7	ABO82270	Pseudomon
24	98.5	12.4	364	7	ABO71177	Pseudomon
25	98.5	12.4	498	7	ABO73227	Pseudomon

26	98.5	12.4	642	7	ABO83358	Pseudomon
27	98.5	12.4	642	7	ABO76021	Pseudomon
28	98	12.3	266	7	ABO81792	Pseudomon
29	98	12.3	2527	7	ADJ70656	Human hea
30	98	12.3	2715	7	ADJ69060	Human hea
31	97.5	12.3	142	7	ABO67968	Pseudomon
32	97.5	12.3	416	7	ABO75829	Pseudomon
33	97.5	12.3	436	7	ABO82371	Pseudomon
34	97.5	12.3	1003	6	ADA54960	Human pro
35	97.5	12.3	1003	6	ABP58226	Human cel
36	97	12.2	317	7	ABO82380	Pseudomon
37	97	12.2	653	7	ABO72672	Pseudomon
38	97	12.2	720	7	ABO83169	Pseudomon
39	97	12.2	781	4	ABG14738	Novel hum
40	96.5	12.2	230	7	ABO80092	Pseudomon
41	96.5	12.2	392	7	ABO82545	Pseudomon
42	96.5	12.2	538	7	ABO72876	Pseudomon
43	96.5	12.2	571	4	AA49765	Human pro
44	96.5	12.2	571	4	AA88393	Human mem
45	96	12.1	260	7	ABO83239	Pseudomon

ALIGNMENTS

RESULT 1
ADO61520
ID ADO61520 standard; protein; 148 AA.
XX ADO61520;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human intermedin SEQ ID NO:2.
XX
KW human; intermedin; hypotensive; gene therapy; hypertension;
KW cardioprotective; diet; prolactin release; growth hormone release;
KW ovarian follicle survival; oedema.
XX
OS Homo sapiens.
XX
PN WO2004048547-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037968.
XX
PR 26-NOV-2002; 2002US-0429327P.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX Hsu SYT;
XX
DR WPI; 2004-441176/41.
DR N-PSDB; ADO61519.
XX
PT New composition comprises an intermedin peptide, useful for treating
PT hypertension, as cardioprotective agent as a diet aid, for the release
PT of prolactin, or for growth hormone release from the pituitary.
XX
PS Claim 1; SEQ ID NO 2; 68pp; English.
XX
CC The invention relates to a novel composition comprising an intermedin
CC peptide, which comprises at least 18 contiguous amino acids in a sequence
CC comprising 148 amino acids (ADO61520). A composition of the invention has
CC hypotensive activity, and may have a use in gene therapy. The composition
CC comprising the intermedin peptide is useful for identifying homologous or
CC related genes, for production of the encoded peptide, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, for gene therapy, mapping functional regions of the protein, or
CC in studying associated physiological pathways. The intermedin peptide is
CC useful for treating hypertension, as a cardioprotective agent, as a diet
CC aid, for the release of prolactin, in growth hormone release from the

Db 70 LPHVGLGRPLLA VVGHPRADRHVRHLQLQCTAVRLQHGPAFPDRAVTRVTOHGAARPA 129

QY 46 SSL-----QPRHPAPRPVVKLHRAALQAGAGLAPVMGQPLRDGGRHSGPRRHSG 97

Db 130 RELVRLRLGREGPRPALRLLSAEYHRP-PATTGHGQ-----RQERAGRHAG 177

QY 98 PRTQAQLRLVGCVLGTQCVQNLHRLWLMGPAQRQDSAPVDPSPSHSYG 148

Db 178 HQHRRAG-----DLGWCRQLQRPRA-RLPSVAAP-----RHPVDPGGLHRPG 216

RESULT 4

ABO82895

ID ABO82895 standard; protein; 362 AA.

XX AC ABO82895;

DT 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa polypeptide #15070.

XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX FN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX DR WPI; 2003-615309/58.

XX DR N-PSDB; ABD16466.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

XX PS Disclosure; SEQ ID NO 31641; 455pp; English.

XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 362 AA;

Query Match 13.6%; Score 108; DB 7; Length 362;

Best Local Similarity 32.9%; Pred. No. 0.083;

Matches 50; Conservative 16; Mismatches 42; Indels 44; Gaps 10;

QY 17 LQLPGSLRSR-----LGGDRPVKVP-----REP---PARSPSS- 47

Db 206 LRLRRNLARTRCAGGLPRPAPGGRQWAPRGRGAPGQPADWRRAPFGGRTPTVAAR 265

QY 48 --LOPHRAPRPVVKLHRAALQAGAGLAPVMGQPLRDGGRHSGPRRHSGPRRTOAOL 105

Db 266 RDLREYGAAPRAIRRRR--RADHGATAA---GGVAGEGQRPASGPRQ---PRRARAQR 317

QY 106 LRVGCVLTGTCQVQNLHRLWLMGPAQRQDSA 137

Db 318 RQAGQV-GKDGQQPQSR--LPGF-GRAPGA 344

RESULT 5

ABO79462

ID ABO79462 standard; protein; 514 AA.

XX AC ABO79462;

DT 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa polypeptide #11637.

XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX FN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX DR WPI; 2003-615309/58.

XX DR N-PSDB; ABD13033.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

XX PS Disclosure; SEQ ID NO 28208; 455pp; English.

XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67825-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 514 AA;

Query Match 13.5%; Score 107.5; DB 7; Length 514;

Best Local Similarity 27.7%; Pred. No. 0.13;

Matches 54; Conservative 11; Mismatches 51; Indels 79; Gaps 11;

QY 20 PGSLSRSI-----GGDPR---PVKPREPPARS-----PSSSLQP-- 50

Db 178 PGRFRALPARLQGTAE DRRGKPGAPAGADPRAYFGFPQRPWRGCRALFGGSLRPAG 237

QY 51 -RHFAFRPVVWKLHRLAQORAGLAPVMGQ-----PLRDGGGQH-----SGPR 93
Db 238 EHEQRE-----CRRAPCQPGVLPAGGQAVHPAARTRTRDELRAAGRRHWLQAPG 290
QY 94 RHSGPRTQQLRVGCVLGT-----CQVQLSHRLWQ-----LMGPAG 132
Db 291 AAVRPGQLARALPAGAALGAGPVFAFPAGPAGCGRRGLSPRLLPQAFRFGLOG-AL 349
* QY 133 RODSA-----PVDPS 143
Db 350 RDDAERGAWPLDFTT 364

RESULT 6
ABO81943
ID ABO81943 standard; protein; 621 AA.
AC ABO81943;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #14118.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD15514.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 30689; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO81943-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 621 AA;
Query Match 13.0%; Score 103.5; DB 7; Length 621;
Best Local Similarity 28.4%; Pred. No. 0.39;
Matches 40; Conservative 13; Mismatches 45; Indels 43; Gaps 7;
QY 31 PRPVKPREPPARSSSSLQPRHPAPRPVWKLHRLAQORAGLAPVMGQPLRDGGR--- 87

Db 421 PDARTQPP-RQWLLAVAPGQRPREV-----ESRPAHRQPALAP--GRPIRRAGALAY 472
QY 88 --CHSGPRRHSGPRRTQAQLRVGCVLGTCCVQNL--SHRLWQL-----127
Db 473 PSEHGARRHADRR-----GTAAQORLAASRALRQHASAAARPAAGNRRRAGD 520
QY 128 MGPAQRQDSAPVDPSPSHSYG 148
Db 521 LPDAGRRHRVHAAAPAPRATG 541
RESULT 7
ABB98398
ID ABB98398 standard; protein; 19938 AA.
XX
AC ABB98398;
XX
DT 05-MAR-2003 (first entry)
XX
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 1.
XX
KW Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;
KW medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
XX
OS Streptomyces viridochromogenes.
XX
PN WO200268436-A1.
XX
PD 06-SEP-2002.
XX
PF 24-AUG-2001; 2001WO-EP009815.
XX
PR 25-FEB-2001; 2001DE-01009166.
XX
PA (COMB-) COMBINATURE BIOPHARM AG.
XX
PI Weitnauer G, Muehlenweg A, Trefzer A, Bechthold A;
XX
DR WPI; 2003-018650/01.
DR N-PSDB; ABZ37515.
XX
PT New avilamycin derivatives, useful for treatment of infections, and
PT nucleic acid encoding avilamycin synthesis enzymes.
XX
PS Example 1; Page 68-301; 319pp; German.
XX
CC The invention relates to avilamycin derivatives (I) with antibacterial,
CC virucide, protozoacide and fungicide activity. (I) are useful for
CC treatment of infections (bacterial, viral, protozoal or fungal), in human
CC or veterinary medicine, particularly where caused by Staphylococcus
CC aureus. (I) are more hydrophilic than known avilamycins. The present
CC sequence is that of an avilamycin synthesis enzyme from the Streptomyces
CC viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
CC ABZ37516)
XX
SQ Sequence 19938 AA;
Query Match 13.0%; Score 103.5; DB 6; Length 19938;
Best Local Similarity 35.3%; Pred. No. 16;
Matches 36; Conservative 7; Mismatches 38; Indels 21; Gaps 5;
QY 18 QLPGLSRSRGDPRPVKPREPPARSSSSLQPRHPA---PRPVWKLHR---ALQARQ 71
Db 8501 EXPTSTVTR---GPPRRPRRPAFPQRRRALGPAVADARFPAAGGLHRCRGAARAGHG 8557
QY 72 AGI-----APVWGQPLRDGGGFGHSGPRRH--SGPRRT 101
Db 8558 RGLHRRGLPQGRPAPLVTLPGRRERTHPXPRRHWTGPRRS 8599
RESULT 8
ABO72835

ID AB072835 standard; protein; 142 AA.
 AC AB072835;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polypeptide #5010.
 XX
 KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX
 PR 27-JUL-1998; 98US-0094190P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 DR N-PSDB; ABD06406.
 XX
 XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 21581; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 142 AA;
 Query Match 13.0%; Score 103; DB 7; Length 142;
 Best Local Similarity 39.3%; Pred. No. 0.09;
 Matches 35; Conservative 6; Mismatches 34; Indels 14; Gaps 7;
 QY 25 RSLGDP---RPVKPRPPARSPSSLSQPRH--PAP-RPVVWKLHRLAQQR-CAGLAP 76
 DB 11 RTGQPAQRALQPRPP---PGACQQRRLPAPERPRPWARRRRRTAGAVRVP 67
 QY 77 VMGQPLRDGGRQHS--PRRHSGPRRTQA 103
 DB 68 -RTQEPQGTFRPGHGRPRPRRAPRA 95
 RESULT 9
 AB075295
 ID AB075295 standard; protein; 417 AA.
 XX
 AC AB075295;
 XX
 DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #7470.
 DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 KW Pseudomonas aeruginosa.
 OS US6551795-B1.
 PN 22-APR-2003.
 XX
 PD 18-FEB-1999; 99US-00252991.
 XX
 PF 18-FEB-1998; 98US-0074788P.
 XX
 PR 27-JUL-1998; 98US-0094190P.
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 DR N-PSDB; ABD08866.
 XX
 XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 24041; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 417 AA;
 Query Match 12.9%; Score 102.5; DB 7; Length 417;
 Best Local Similarity 27.9%; Pred. No. 0.32;
 Matches 36; Conservative 8; Mismatches 58; Indels 27; Gaps 3;
 QY 20 PGS-LRSRLGDPREPKPREPPARSPSSLSQPRHPPAPRPVWKLHRLAQQRGAGLAPV 78
 DB 216 PGSGTHRALVGDHPHPAGSRADAAPPQORAAHPAPVPCFARRRLSTGGGGKPGRRFFGI 275
 QY 79 -----GQPLRDGGRQHSGRPRRHSGPRRTQAQLLRVGCVLGTCQVQNLHSLRLWQLMGFAG 132
 DB 276 PRSAPPGHFVSRGPPDPGDFRPLHPR-----AQQRRRRAPP 315
 QY 133 QDSAPVDP 141
 DB 316 PGRLLPVR 324
 RESULT 10
 AAY96318
 ID AAY96318 standard; protein; 242 AA.
 XX
 AC AAY96318;
 XX
 DT 17-AUG-2000 (first entry)

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, PT
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 30948; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX SQ Sequence 327 AA;

Query Match 12.7%; Score 101; DB 7; Length 327;
Best Local Similarity 30.2%; Pred. No. 0.34;
Matches 54; Conservative 15; Mismatches 58; Indels 52; Gaps 11;
QY 11 CISLLCQLPGSLERSLGGDPRPVK-----PREPPARSPSS----- 46
DB 55 CLPLRRRTGTAAGQPGDGPAPKVAAGRPPVAVLCRAPRLAPGAPGAGDRGR 114
QY 47 ----SLQPHFA----PPVVKLHRA-IQORAGLIA--PWGQPIRDGGQHSQ--PR 93
DB 115 GRALSQRPRRAAGQPEQF-----HRAGLRARRAAGLACPFATSRRLAAGRRGVHGLHPA 169
QY 94 RHSG-----PRRTQAQLRVGCVLTGTCQVONLSHRLWLMGFPAGRODSAPVD---PSSP 144
DB 170 VEPGLYQPTIDRAALVRQVLRFPCRCARLRPRRTAAVAG-AGRA-ARFVDGQWFGAP 226

RESULT 13
ABO69540
ID ABO69540 standard; protein; 528 AA.
XX
AC ABO69540;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #1715.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD03111.
XX

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, PT
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 18286; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX SQ Sequence 528 AA;

Query Match 12.7%; Score 100.5; DB 7; Length 528;
Best Local Similarity 28.0%; Pred. No. 0.63;
Matches 47; Conservative 9; Mismatches 43; Indels 69; Gaps 9;
QY 28 GGDPRPVK-----REPPARSPSSIQ---PRHPAPRVVWKLHREAL 66
DB 52 GDDEVAADPRRGAWLPAGHPAGGADLQPAALFGLALHLRVPRHPAVHVAVLHRRLL 111
QY 67 QAQ-----RGAGLAPVMGOPLR--DGG-----ROHSGPRRHSGPRRT 101
DB 112 QPECHTRPGLSQRVLPRRLQHGAGLRP---QHLRHDGNTLRRRDOEHAPRRSGSGARLR 168
QY 102 QAQL-----LRVGCVLGTGTCQVONLS-----HRLWQLMGPA 131
DB 169 HGRHLPLPAHRPALGAAPGTAVLQQRSDPDAAFAHLGGVHR--HSAGPA 214

RESULT 14
ABO77087
ID ABO77087 standard; protein; 464 AA.
XX
AC ABO77087;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #9262.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD10658.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 XX pathological conditions resulting from bacterial infection.
 PT Disclosure; SEQ ID NO 25833; 455pp; English.

XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 CC Sequence 464 AA;

Query Match 12.6%; Score 100; DB 7; Length 464;
 Best Local Similarity 28.4%; Pred. No. 0.61;
 Matches 42; Conservative 13; Mismatches 47; Indels 46; Gaps 9;

QY 29 GDP-RPVK-----PREPARSPSSLOPRHPA-----PRPVVKLHRLAQAQGA 72
 DB 185 GDHPFGRRVPGPADAPAAAGRGDQPRQGDHGAAGAAVAGHPAPAVIRHLSGRHRGP 244
 QY 73 GLAPVVGQPLR-----DGRHSGPRHSGPRRTQAQLLRVGCVLGTQCVONLS 121
 DB 245 ARGP--RRPVQRAGDAPAPDPGRH---RRGNGLRR--RQLPR-----PVEGTD 290
 QY 122 HRLW-----QLMGPAQDSAPVDPSF 144
 DB 291 RRAWPGRRHLEPPGRRGHPAVHPGPF 318

RESULT 15
 ABG16571
 ID ABG16571 standard; protein; 555 AA.

XX AC ABG16571;
 XX 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #16562.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.

XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSR-) HYSRQ INC.

XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX N-PSDB; AAS80758.

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 46930; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 555 AA;

Query Match 12.6%; Score 100; DB 4; Length 555;
 Best Local Similarity 31.0%; Pred. No. 0.74;
 Matches 35; Conservative 10; Mismatches 48; Indels 20; Gaps 5;

QY 37 REPARSPSSLOPRHPAPRPVVKLHRLAQAQGAQLAPVVGQPLRDGGRHS-----G 91
 DB 10 RAPPPFAPKSSRQFAPLAPRP--WSSRARLPRSRPSAIPPGWG---RAGKDSAGWCAGG 64
 QY 92 PRHSGPRRTQAQLLRVGCVLGTQCVONLSHR-----LWQLMGPAQGRQDSAP 138
 DB 65 P-----APRATHAPSQQLGADGPEAVAQDTERRLGPPTALWPRAERPGRGDASP 113

Search completed: October 22, 2004, 08:51:09
 Job time : 158 secs

A;Accession: C86301
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-414 <SPO>
A;Cross-references: UNIPROT:Q9SEE9; GB:AE005172; NID:9999058; PIDN:AAG10821.1; GSPDB:GN
C;Genetics:
A;Map position: 1

Query Match 11.8%; Score 93.5; DB 2; Length 414;
Best Local Similarity 30.7%; Pred. No. 1.6;
Matches 42; Conservative 13; Mismatches 51; Indels 31; Gaps 7;

QY 20 PGSLSRLSGDPRPVKPREPPARSPSSSLQPRHPAPRVVWKLHRLALQAGAGLAPVMG 79
Db 254 PGSPPIRRRGDTP-----PRRPA-SPSRGRSPSPPPR-----RYRSPRGGSP-RRIRG 300

QY 80 QPLRDGG-----RQSGPRHSGPRRTQALLRVGCVLGTQVQNLHRLWQL 127
Db 301 SPVRRSPLPLRRSPPPRLRSPRRSPRRSPRRP-----GRSRSSISPRKGR- 355

QY 128 MGPAGRQDSAPVDPSSP 144
Db 356 -GPAGRGRSSYS SSP 371

RESULT 3
S10889
proline-rich protein - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S10889
R;Lyons, K.M.; Stein, J.H.; Smithies, O.
Genetics 120, 267-278, 1988
A;Title: Length polymorphisms in human proline-rich protein genes generated by intragenic
A;Reference number: S02127; MUID:89121440; PMID:2851479
A;Accession: S10889
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-309 <LYO>
A;Cross-references: UNIPROT:Q04118; EMBL:X07881; NID:935637; PIDN:CAA30728.1; PID:929666
C;Genetics:
A;Introns: 22/1; 34/1
C;Superfamily: proline-rich protein

Query Match 11.5%; Score 91.5; DB 2; Length 309;
Best Local Similarity 27.3%; Pred. No. 1.8;
Matches 35; Conservative 13; Mismatches 63; Indels 17; Gaps 3;

QY 20 PGSLSRLSGDPRPVKPREPPARSPSSSLQPRHPAPRVVWKLHRLALQAGAGLAPVMG 79
Db 188 PQGNSQSGPPRRPGKEGPP---PQGGNSQSGPPRRPGKEGSPSQGGNKPRGPPPHG 244

QY 80 QPLRDGGRHSGPRRSGPRRTQALLRVGCVLGTQVQNLHRLWLMGPAQDSAPV 139
Db 245 KPQGPFPQEGNKQRPDPPPRRPQGGPPG-----NPQQLPPPPACKPQGPFP 292

QY 140 DPSS--PH 145
Db 293 PPQGRPH 300

RESULT 4
A36298
proline-rich protein PRB3M (null) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36298
R;Azren, E.A.; Minaguchi, K.; Latreille, P.; Kim, H.S.
Am. J. Hum. Genet. 47, 686-697, 1990
A;Title: Alleles at the PRB3 locus coding for a disulfide-bonded human salivary proline-
A;Reference number: A36298; MUID:91022705; PMID:2171329
A;Accession: A36298
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA
A;Residues: 1-220 <AZE>
A;Cross-references: UNIPROT:Q7M4M9
C;Genetics:
A;Gene: GDB:PRB3
A;Cross-references: GDB:119513; OMIM:168840
A;Map position: 12p13.2-12p13.2
C;Superfamily: proline-rich protein

Query Match 11.5%; Score 91; DB 2; Length 220;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 41; Conservative 7; Mismatches 56; Indels 20; Gaps 6;

QY 18 QLFGLSRLSGDPRPVKPREPPARSPSSSLQPRHPAPRVVWKLHRLALQAGAGLAPV 77
Db 68 QPFGGNSQSGPPRRPGKEGPP---PQGGNSQSGPPRRPGKEGPPQGGNSQSGPPPR 124

QY 78 MQQ---PLRDGGRHSGPRHSG-PRRTQALLRVGCVLGTQVQNLHRLWLMGP--- 130
Db 125 PGKEGPPPPQGGNSQSGPPRRPGKEGPPQ-----GGNSQSGPPRRPGKEGPPQ 176

QY 131 AGRQDSAPVDPSSP 144
Db 177 GGNQSGP--PPRP 188

RESULT 5
B55663
oligodendrocyte-specific proline-rich protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: B55663; A55663
R;Yamamoto, Y.; Mizuno, R.; Nishimura, T.; Ogawa, Y.; Yoshikawa, H.; Fujimura, H.; Adachi,
J. Biol. Chem. 269, 31725-31730, 1994
A;Title: Cloning and expression of myelin-associated oligodendrocytic basic protein. A r
A;Reference number: A55663; MUID:95081123; PMID:7989345
A;Accession: B55663
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-170 <YAM>
A;Cross-references: UNIPROT:Q63327; GB:D28110; NID:9644501; PIDN:BAA05657.1; PID:d10062
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-68, 'RTV' <YA2>
A;Cross-references: GB:D28111; NID:9644502; PIDN:BAA05658.1; PID:d1006203; PID:g1408058

Query Match 11.3%; Score 90; DB 2; Length 170;
Best Local Similarity 40.3%; Pred. No. 1.4;
Matches 29; Conservative 2; Mismatches 35; Indels 6; Gaps 4;

QY 31 PRPVKPREP--PARSPSSSLQPRHPAPRVVWKLHRLALQAGAGLAPVMGQPLRDGGRQ 88
Db 100 PRPAKPRSPPIPAKPSRSPETERQPRPREV-RPPPAKQKPPQKSKQPARSSPLRGFTS 158

QY 89 HSG-PRRHSGPR 99
Db 159 RGGSPTR--APR 168

RESULT 6
E30411
synapsin Ia - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 01-Dec-2000
C;Accession: E30411; F30411; A35758
R;Suedhof, T.C.; Czernik, A.J.; Kao, H.T.; Takei, K.; Johnston, P.A.; Horiuchi, A.; Kan
Science 245, 1474-1480, 1989
A;Title: Synapsins: mosaics of shared and individual domains in a family of synaptic ve
A;Reference number: A30411; MUID:89388265; PMID:2506642
A;Accession: E30411
A;Status: preliminary
A;Molecule type: mRNA

Query Match	11.1%;	Score 88;	DB 2;	Length 304;
Best Local Similarity	27.8%;	Pred. No. 3.4;		
Matches	37;	Conservative 17;	Mismatches 59;	Indels 20; Gaps 5;
Qy	19	LPGLSRSLGDDPRPVKREPPA	---RPSSSSIOPHPAPRPVVKLHRALOAQRGAGLA	75
Db	41	LPGLSSAATGSRCPVRGRPPSGARRGASRWWRRPPCQSPPCWATHRPQGRQPSG-S	99	
Qy	76	PVMQCPALDGGCRQHSGRHRHSGRPTQALLRVGCVLGTCCQVQLSHRLWLMGP	-----130	
Db	100	PSDGLP-RTAHTSRCCPACQSRGRTEWKRPAC	-----SERGMVPVGDPDPAN	148
Qy	131	AGRODSAPVDFSS	143	
Db	149	SGLEPNPVPVPRSS	161	

	Query Match	11.0%; Score 87.5; DB 2;	Length 308;
	Best Local Similarity	27.5%; Pred. No. 3..7;	
	Matches 39; Conservative 15;	Mismatches 39;	Gaps 8;
Qy	22 SLRSLSGDDPRVKPREPASP-SSSLOPRAPRPVWKHLRALQAQRAGLAPVMQG 80 : :	 :::	:
Dd	4 SASRSDGGD--PLRPASFLRSPFVDGDPLRPA-----SPRLRS 41 : :	 :::	:
Qy	81 PLRDGRHSGRRHSPPRTAQALLRVSCVLG-TCOVNLSHRLWOLMGPAQRDS--- 136 : : : : : :	: : : : : : : : : :	:
Dd	42 FVSDDG----DLRPASP-RLSRPLCASFPVGLTAYLEQVRTGVMDI--PAGYLPADYF 94 : : : : :	: : : : : : : : : :	:
Qy	137 -----ApvDPSS 143 		
Dd	95 EGITWAGGVAVLLPFQVPDPS 116 		

RESULT 10
S75327

Query Match	10.8%;	Score 86;	DB 2;	Length 383;	
Best Local Similarity	27.4%;	Pred. No. 6;			
Matches	48;	Conservative 11;	Mismatches 34;	Indels 82;	Gaps 11;
Qy	11	CISILCLQLPCLSLERSLGGDPRPVKP--RPPPA-RSPSSSIQRPHPAPRPVWKLHREALQ	67		
Db	92	CPSLCPSEEPGT-----SGTEPLGPASRRPFGRLSPVVKPK-----E	131		
Qy	68	AQRGAGL--AP-----VMGQPLRDGGRQHSQPRR-----	94		
Db	132	CLRGATLGAQAPESRGQGHLLVPRPVGQP--EGPRQPGRPQRPVPRPFGLOSQPGCPPE	189		
Qy	95	-----HSGPRRTQALLRVGCVLTGTCQVQNLSHRLWLQMLMGPAQRQDSAPVDPPSP	144		
Db	190	GTLGWPSPPFLQARASPSRRGASLGP-QVO--PHR-----DPSGF	225		

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